

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OK protein - nucleic search, using frame_plus.p2n model

Run on: December 9, 2002, 12:23:04 ; Search time 2719 Seconds
(without alignments)
3574.968 Million cell updates/sec

Title: US-09-765-034-2
Perfect score: 1747
Sequence: 1 MCGTMANNATCKMFLAAEA.....KSLTFSKRAHELLSFRER 334

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2.1/USPNO.spool/US09765034/runat_05122002.132015.21439/app_query.fasta.1.519
-DB=GenEmbl -GENE=fastap -SUPFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09765034.BCGN.1.1.1616.runat.05122002.132015.21439 -NCPG=6 -ICPU=3
-NO.XLPHY -NO.MAP -LARGOQUERY -NEG.SCORES=0 -WAIT -LONGLOG -DEV.TIMEOUT=120
-WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vl:*
30: em_hlg_hum:*
31: em_hlg_inv:*
32: em_hlg_other:*
33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rtd:*
36: em_hlg_mam:*
37: em_hlg_vrt:*
38: em_sy:*
39: em_hlgo_hum:*
40: em_hlgo_mus:*
41: em_hlgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1737	99.4	1325	9	AF247785 Homo sapi
2	1737	99.4	1380	9	AF348078 Homo sapi
3	1737	99.4	1449	9	BC030948 Homo sapi
4	1737	99.4	1542	6	AX342665 Sequence
5	1725	98.7	1996	6	AR035943 Sequence
6	1713	98.1	90343	9	AC116026 Homo sapi
7	1713	98.1	132745	9	AC068647 Homo sapi
8	1708	97.8	158144	2	AC016455 Homo sapi
9	1231.5	69.6	15543	6	AX376573 Sequence
10	1215.5	69.6	1598	10	AF295367 Mus muscu
11	861	49.3	60298	2	AC116149 Mus muscu
12	727.5	41.6	60298	2	AC116149 Mus muscu
13	504	28.8	3204	10	RN022830 Rattus norv
14	500	28.6	1293	10	U22829 Rattus norv
15	500	28.6	12630	10	U22829 Rattus norv
16	500	28.6	288763	2	AC124692 Mus muscu
17	499.5	28.6	2951	5	AF323354 Xenopus l
18	498	28.5	1312	9	HS042030 Human p2y1
19	498	28.5	1426	9	HS042029 Human p2y1
20	498	28.5	1498	5	GDATPREC Human p2y1
21	498	28.5	2424	9	HS042030 Human p2y1
22	498	28.5	16178	9	HS042029 Human p2y1
23	498	28.5	73949	2	AC105795 Rattus no
24	498	28.5	176170	2	AC021662 Homo sapi
25	498	28.5	176251	9	AC013251 Homo sapi
26	495.5	28.4	1308	4	BT034041 Bos taurus
27	495.5	28.4	1666	4	BT034041 Bos taurus
28	494	28.3	1180	5	MG009842 Melagris g
29	494	28.3	1192	5	AF012103 Melagris g
30	493.5	28.2	2231	5	AF242850 Raja erin
31	485.5	27.8	3055	9	HSATPRMR Z43205 H. sapiens m
32	485.5	27.8	3055	11	G28604 human STS S
33	477	27.3	1014	6	AX148186 Sequence
34	477	27.3	1014	6	AX305130 Sequence
35	477	27.3	1014	6	AX379468 Sequence
36	477	27.3	1014	6	AX384211 Sequence
37	477	27.3	1014	6	AX464561 Sequence
38	477	27.3	1014	6	AB083598 Homo sapi
39	477	27.3	1014	6	AF411109 Homo sapi
40	477	27.3	1081	6	AX458238 Sequence
41	477	27.3	1092	9	AF370886 Homo sapi
42	477	27.3	1414	9	AB065877 Homo sapi
43	477	27.3	9905	6	AX379470 Sequence
44	477	27.3	67645	9	AL356486 Human DNA
45	477	27.3	156555	9	AC026756 Homo sapi

RESULT 1

ALIGNMENTS

LOCUS	AF247785	1325 bp	mRNA	linear	PRI 26-MAR-2002
DEFINITION	Homo sapiens P2Y purinoceptor 1 mRNA, complete cds.				
ACCESSION	AF247785				
VERSION	AF247785.1	GI:19716154			
KEYWORDS					
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1325)				
TITLE	Zhang, W., Li, N., Wan, T. and Cao, X.				
JOURNAL	Human P2Y purinoceptor 1				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 1325)				
TITLE	Zhang, W., Li, N., Wan, T. and Cao, X.				
JOURNAL	Direct Submission				
FEATURES	Submitted (21-MAR-2000) Department of Immunology, Second Military Medical University & Shanghai Brilliance Biotechnology Institute, 800 Xiangyin Rd., Shanghai 200433, P.R. China				
SOURCE	Location/Qualifiers				
CDS	1..1325				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	69..1073				
	/codon_start=1				
	/product="P2Y purinoceptor 1"				
	/protein_id="AA195690.1"				
	/db_xref="GI:19716155"				
	/translation="MGLMAMNATCKMWAALAEALAEKYIISIFGIEFVYVAGNTIVVTGIFSLKMNSSNITLFLNSLDLFLCTLPMLISVANGMTYDVLCTSRVYLHANIYTLIFETISIDRYLILIKYFHEHLQKKEFALLSLAIWVLTLELPILINPVTINGTCTNDPFGSDPNVNLIVSMCLTLLGLPILEVMGFYKIALFLKQNRFOVATLPLEKPLNLVTMAVIVESVLETPYHVMNRVIAISGSKOCTOVYINSEYIVRPLAFINSVINPVFYFLGDHFRDMLMNRHNFKSLTSPRAHEHLLSFRKK"				
BASE COUNT	359 a 292 c 261 g 413 t				
ORIGIN					
Alignment Scores:					
Pred. NO.:	2.94e-132	Length:	1325		
Score:	1737.00	Matches:	333		
Percent Similarity:	99.70%	Conservative:	0		
Best Local Similarity:	99.70%	Mismatches:	1		
Query Match:	99.43%	Indels:	0		
DB:	9	Gaps:	0		
US-09-765-034-2 (1-334) x AF247785 (1-1325)					
OY	1 MetleuglyllemeAlaTTPasolaLhrcysysAsnTPLeuAlaAGLUALaA 20				
Db	69 ATGCTGGGAGATCGCATGAGATGCAACTTGGCAAAAAGCTGGCGAGAGGCTGCC 128				
OY	21 LeugluysTYTYTYLeuSerIllePheTYrglylIleGluPheValAlaGlyVValleugly 40				
Db	129 CTGGAAAGAGTACTACCTTCATTTTATATGAGGATGAGTTCGTTGTGGAGTCTTGGGA 188				
OY	41 AsnThrIleValAlaTYrglylTYrIllePheSerleuLysAsnTPasnsrSerAsnIle 60				
Db	189 AATACCATTTGTTTACGGCTACATCTTCTCTGGAGAACTGGAAACAGCAAGTAATATT 248				
OY	61 TYrLeuPheAsnLeuSerValSerAspLeuAlaPheLeuCYSThrLeuProMetleuIle 80				
Db	249 TATCTCTTAACCTCTCTGCTCTGACTTACCTTTTCTGTGCACCCCTCCCATGCTGATA 308				
OY	81 ArgSerTYrAlaAsnGlyAsnTPrlleTYrglyAspValleuCYsIleSerAsnArgTYr 100				
Db	309 AGGAGTTATGCCAATGCAAACTGATATATGAGACGTCGTCCATTAAGCAACCGATAT 368				
OY	101 ValIeuHsAlaAsnLeuTYrThrSerIlleLeuPheLeuThrPheIleSerIlleAspArg 120				
Db	369 GTGCTTATGCCAACCTGTATACAGCACTTCTCTTCTTGCATCTTATATCAGCATGATCGA 428				

QY	121	TYRLEUILLILEUYSYRPROPHENARGUHLSTLEULEGILYSLYSGLUPHEALILE	140
Db	429	TACTTGATATTATAGATATCTTTCCGAGAACACCTTCTCGAAAGAAAGATTGCTATT	488
QY	141	LEUILLSEULEALALETRPVALLLEUVALTHRLLEUGILDEULEUPROILLEUPROLEU	160
Db	489	TTAATCTCTTGSGCAATTTGGGTTTTAGTAACTTAGATTTACTACCTACTTCCCTT	548
QY	161	ILEASNPROVALILETHRASPANGLYTHRHRCYASNASPPHEALASERSEGLYASP	180
Db	549	ATTAATATCCGTATATACATGACATGACACACCTGTAATGATTTGGCAAGTCTGGAGAC	608
QY	181	PROASNTRYASNLEULEILEYRSEMETCYSLSEUTHRLLEULEGILYRHEULEILEPROLEU	200
Db	609	CCCACTACCAACCTCATTTTACAGCAGATGTCATACACGTGTGGGTCCTTATTCCTCTT	668
QY	201	PHENALMETCYSPHETHRYTYRYSILEALALEUPHEULEYSGILNARGASNRGILN	220
Db	669	TTTGATGATGTCTTCTTTATTACAAAGATGGCTCTCTCTCTTAAGCAGAGAAATGGCAG	728
QY	221	VALALATHRLALEUPROLEUGILYUSPROLEUASNLEUVALILEMETALAYALVALILE	240
Db	729	GTTCGTACTGCTGCTGCCCTTGAAAAAGCCTCAACTTGTCATGATGCGATGGAAATC	788
QY	241	PHESERVALPROPHETHRPROTYRHRHSVALMETALGASRYVALARGILEALASERARGLEU	260
Db	789	TTCTCTGTGCTTTTATACACCTCATACGTCATGCGGAAATGTAGATATCCTTTACAGCCCG	848
QY	261	GLYSERTPLYSGLITTYRGLINCYSRHRGILVALILEASNSEPHETHRYLLEVALTHR	280
Db	849	GGGAGTTGGAACCATATCATGACGTACGTACGTGCGTCATCAATCCTTTTACTTTGTGACA	908
QY	281	ARGPROLEUALAPHELEUASNSEVALILEASNPROVALPHERTYRPHLEULEUGILYASP	300
Db	909	CGGCTTTGGCCTTTCTGTGACAGTGTCAATCAACCTGCTCTTATTTCTTTGGGAGAT	968
QY	301	HISPHETGASPHETLEULEMETASNGLINEUARGHLSAANPHYSERLEUTHRSEPHLE	320
Db	969	CACCTTCAGGACATCTGTATGATACATGACGACACCACTTCAAAATCCCTTACATCCCTTT	1028
QY	321	SERATGTPALAHISGILDEULEULEUSERPHEARGILYUS	334
Db	1029	AGCAGATGGGCTCATGAACTCCTACTTTCATTCACAGAAAAAG	1070
RESULT 2	AF348078	1380 bp	linear
LOCUS	AF348078		PRI 03-APR-2001
DEFINITION	Homo sapiens G-protein coupled receptor 91 (GPR91) mRNA, complete cds.		
ACCESSION	AF348078		
VERSION	AF348078.1	GI:13517982	
KEYWORDS			
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1380)		
TITLE	Wittenberger,T., Schaller,H.C. and Hellebrand,S.		
FEATURES	An expressed sequence tag (EST) data mining strategy succeeding in the discovery of new G-protein coupled receptors		
JOURNAL	J. Mol. Biol. 307 (3), 799-813 (2001)		
MEDLINE	J. Mol. Biol. 307 (3), 799-813 (2001)		
PUBMED	11273702		
REFERENCE	2 (bases 1 to 1380)		
AUTHORS	Wittenberger,T., Schaller,C.H. and Hellebrand,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (08-FEB-2001) ZMNH, Institut fur Entwicklungsneurobiologie, Martinistr. 52, Hamburg 20246, Germany		
FEATURES	location/Qualifiers		
source	1..1380		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/chromosome="3"		

gene /map="3q24-q25.1"
 1.1380
 /gene="GPR91"
 55.1047
 CDS /gene="GPR91"
 /note="Orphan receptor"
 /codon_start=1
 /product="G-protein coupled receptor 91"
 /protein_id="AAK29080.1"
 /db_xref="GI:13517983"

BASE COUNT 383 a 294 c 274 g 429 t
 ORIGIN
 /translation="MAMNATCKNMLAEALAEKYYLSIFGYIEFVVGNGITIVYGY
 /translation="MAMNATCKNMLAEALAEKYYLSIFGYIEFVVGNGITIVYGY
 IFSKNNMSSNIYLFNVSDFLCTPMLIRSYANGNMIYGVLCISNRVLANL
 YTSILFEFISIDRLIIRKPREHLIOKKEPALISIAIWIYVLELILPLILANL
 ITDNGTCNDPAGSDGDPYNNLISWCLLLEFLIFPYMCEPYKYLAFIKORNOVA
 TALDLKPLNVIKAVIVFVLETPYHVMNRNKLASRLGSMKQICTOVVINSFIVT
 RPLAFNSVINPVEFELGDHFRDMLNMRNFKSLTFSFMHELLSFERK"

Alignment Scores:
 Pred. No.: 3.07e-132 Length: 1380
 Score: 1737.00 Matches: 333
 Percent Similarity: 99.70% Conservative: 0
 Best Local Similarity: 99.70% Mismatches: 1
 Query Match: 99.43% Indels: 0
 DB: Gaps: 0

US-09-765-034-2 (1-334) x AF348078 (1-1380)

Oy 1 MetLeuGlyIleMetAlaTrpPasnAlaThrCysLysAsnTrpLeuAlaIleAlaIa 20
 Db 43 ATGCTGGGGATCATGCAATGCAATGCACTTGCAGCAAGAGCTGCC 102
 Oy 21 LeuGluLysTyrTyrLeuSerIlePheTyrGlyIleGluPheValaIglValLeuGly 40
 Db 103 CTGGGAAAGTACTACCTTCCATTTTATGGAGTACTGCTGGAGAGCTTGA 162
 Oy 41 AsnThrIleValIValTyrGlyTyrIlePheSerLeuLysAsnTrpAsnSerAsnIle 60
 Db 163 AATACCATGTTGGTTTACGGCTACATCTCTCTGMAAAGCTGGAACAGCATATAT 222
 Oy 61 TyrLeuPheAsnLysSerValSerAspLeuAlaPheLeuCysThrLeuProMetLeuIle 80
 Db 223 TATCTCTTAACTCTCTCTCTCTGACTTCTCTGCAACCTCCCGCATGCGATA 282
 Oy 81 ArgSerTyrAlaAsnGlyAsnTrpIleTyrGlyAspValLeuCysIleSerAsnArgTyr 100
 Db 283 AGGAGTATGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 342
 Oy 101 ValLeuHisAlaAsnLeuTyrThrSerIleLeuPheLeuThrPheIleSerIleAspArg 120
 Db 343 GTGCTTCATGCAACCTCATATACAGCATCTCTCTCTCTCTCTCTCTCTCTCTCT 402
 Oy 121 TyrLeuIleIleLysTyrProPheArgLysIleLeuGlnLysLysGluPheAlaIle 140
 Db 403 TACTGTAT 462
 Oy 141 LeuIleSerLeuAlaIleTyrValLeuValThrLeuGlnLeuLeuProIleLeuProLeu 160
 Db 463 TTAACCTCTGCGCATTTGGCTTTAGTAACCTTACTACTACTACTACTACTACTCT 522
 Oy 161 IleAsnProValIleThrAspAsnGlyThrPheCysAspAspPheIleSerGergLysAsp 180
 Db 523 ATTAATCCCTGTTATATACATGACACCACTGTATATATATATATATATATATAT 582
 Oy 181 ProAsnTyrAsnLeuIleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIleProLeu 200
 Db 583 CCCAATCAACCTCATTTAGAGCATGTGTAAACACTGTGGGCTTCTTATCTCTCT 642
 Oy 201 PheValMetCysPhePheTyrTyrIleAlaLeuPheLeuLysGlnArgAsnArgGln 220
 Db 643 TTTTGATGTGTCTTTTATATACAAAGATTGCTCTCTCTCTCTCTCTCTCTCTCTCT 702

Oy 221 ValAlaThrAlaLeuProLeuGluLysProLeuAsnLeuValIleMetAlaValIle 240
 Db 703 GTTGTACTACTGCTCTGCCCTTGAAGACCTCTCACTGTGTCATGAGAGTGAATC 762
 Oy 241 PheSerValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeu 260
 Db 763 TTTCTGTGTGTTTATACCCCTATCAAGTCATCGGAGATGTAGANTCGTTACCCCT 822
 Oy 261 GlySerTrpLysGlnTyrGlnCysThrGlnValIleIleAsnSerPheTyrIleValThr 280
 Db 823 GGGAGTGGAGACAGTATAGTACACTGAGTGTGTCATCAACTCTTTTACATGTGACA 882
 Oy 281 ArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAsp 300
 Db 883 CGGCTTTGGCTTTCTGAAACAGTGTATCAACCGCTCTTATTTCTTTGGAGAT 942
 Oy 301 HisPheArgAspMetLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 320
 Db 943 CACTTACGGACATGCTGATGATCAATCACTGACACACACTTCAATCCCTTACATCTTT 1002
 Oy 321 SerArgTrpAlaHisGluLeuLeuLeuSerPheArgGluLys 334
 Db 1003 AGCAGATGGGCTCATGACTCTTCTTATTCAGAGAAAG 1044

RESULT 3
 LOCUS BC030948 1449 bp mRNA linear PRI 13-JUN-2002
 DEFINITION Homo sapiens, G protein-coupled receptor 91, clone MGC:32514
 IMAGE:4594810, mRNA, complete cds.
 ACCESSION BC030948
 VERSION BC030948.1 GI:21410927
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euteria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1449)
 AUTHORS Strusberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK
 COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: CLONTECH
 CDNA Library Preparation: CLONTECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www-shgc.stanford.edu>
 Contact: (Dickson, Mark) mdedpaxill.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

FEATURES
 source
 1..1449
 /organism="Homo sapiens"
 /db_xref="LocusID:56670"
 /db_xref="taxon:9606"
 /clone="MGC:32514 IMAGE:4594810"
 /tissue_type="kidney"
 /clone_11b="NIH_MGC_75"
 /lab_host="DH10B"
 /note="Vector: pDNR-LIB"
 100..1104
 /codon_start=1

CDS
 100..1104
 /codon_start=1

Db 438 AGGAGTTATGCCAATGGAACCTGATATATGAGAGCTGCTCGCTAAAGCAACCATAT 497
 QY 101 VALLLEHIALAAsnleuTyThrSerileuPheleuThrpheleuSerileaspArg 120
 |||||
 Db 498 GTGCTTCATGCACACCTCATATACACGACATTCCTTCTCATTATTCAGCATAGATCGA 557
 QY 121 TYRLEUlleileuTyThrProPheArgGluHisleuGlnLysGluPheAlaIle 140
 |||||
 Db 558 TACTGATATTAAGTATACCTTCCGAGAACCTTCCTCAAAAGAAAGATTGCTATT 617
 QY 141 LeuileSerleuAlaIleTrpValleuValThrleuGlnleuProilleuProleu 160
 |||||
 Db 618 TTAATCTCTTGCCCATTTGGGTTTATGACCTTACAGTTACTACCATCTCCCTT 677
 QY 161 IleasnProvalIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyasp 180
 |||||
 Db 678 ATAAATCCTGTTATACATGACATGACACACCTGTAATGATTTCGCAAGTTCTGAGAC 737
 QY 181 ProAsnTyraAsnleuIleuTySerMetCysleuThrleuGlnlyPheleuIleProleu 200
 |||||
 Db 738 CCCAATCAACCTCATTTACAGCATGTGTACACCTGTGGGTTCTTATCTCTT 797
 QY 201 PheValMetCysPhePheTyThrIleAlaIlePheleuPheleuGlnIleArgAsnArgGln 220
 |||||
 Db 798 TTTTGATGTGTTCTTTATTAACAGATTGCTCTCTTCCTAAGCAGAGAAATGAGCAG 857
 QY 221 ValAlaThrAlaIleuProleuGlnLysProleuAsnleuValIleMetAlaValAlaIle 240
 |||||
 Db 858 GTTGCTACTGCTCGCCCTTGAAAGCCTCTCAACTGTGTATCATGAGCAGGTGATAC 917
 QY 241 PheSerValProPheThrProTyraHisValMetArgAsnValArgIleAlaSerArgleu 260
 |||||
 Db 918 TTCTCTGCTCTTTTACACCTATACGTCATGCGGAATGTGGAGTCCCTTACCCCTG 977
 QY 261 GlySerTrpLysGlnTyraGlnCysThrGlnValIleAlaSerPheTyThrIleValThr 280
 |||||
 Db 978 GGGAGTGGAAACAGTATAGTCACATGCGTCGTCATCACTCTTTTACATGTGAGCA 1037
 QY 281 ArgProleuAlaPheleuAsnSerValIleasnProvalPheTyThrPheleuGlnIleasp 300
 |||||
 Db 1038 CGGCTTTGGCTTCTTCTGAAGTGTATCAACACCTGCTTCTATTTCTTTGGAGAT 1097
 QY 301 HisPheArgAspMetleuMetAsnGlnleuArgHisAsnPhelYserleuThrSerPhe 320
 |||||
 Db 1098 CACTTCAGGACATGCTGTATGATCAACAGACACACACTTCAAAACCTTACATCTTT 1157
 QY 321 SerArgTrpAlaHisGlnleuLeuLeuSerPheArgGlnLys 334
 |||||
 Db 1158 AGCAGTGGGCTCATGACTCTTACTTTTCAATTCAGAGAAAG 1199

RESULT 5
 LOCUS AR035943 1996 bp DNA linear PAT 29-SEP-1999
 DEFINITION Sequence 1 from patent US 5871963.
 ACCESSION AR035943
 VERSION AR035943.1 GI:5952611
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 1996)
 AUTHORS Conley,P.B. and Jantzen,H.-M.
 TITLE P2u2 putative ligand receptor and nucleic acid encoding the receptor
 JOURNAL Patent: US 5871963-A 1 16-FEB-1999;
 FEATURES
 source 1. 1996
 /organism="Unknown"
 BASE COUNT 513 a 455 c 381 g 647 t
 ORIGIN

Alignment Scores: 4.3e-131 Length: 1996
 Pred. No.: 1725.00 Matches: 331
 Score:

Percent Similarity: 99.108
 Best Local Similarity: 99.108
 Query Match: 98.748
 DB: 6 Gaps: 0
 US-09-765-034-2 (1-334) x AR035943 (1-1996)
 QY 1 MetleuGlyLleMetAlaThrPheAsnAlaThrCysLysAsnTrpPheAlaIleAlaIleAla 20
 |||||
 Db 625 ATGCTGGGATTCATGGCATGATGCACTTGCAAAAGCTGGGAGAGAGGGCTGCC 664
 QY 21 LeuGlnLysTyThrIleuSerIlePheTyGlyIleGluPheValAlaGlyValleuGly 40
 |||||
 Db 685 CTGGAAAGATCACTACCTTCCATTTTATGGATGAGTTCCTGTGGAGTCCCTGGA 744
 QY 41 AsnThrIleValValTyraGlyTyThrIlePheSerleuLysAsnTrpAsnSerSerAlaIle 60
 |||||
 Db 745 AATACATGCTGTTTAAAGGCTATCTCTCTGTGAAGAACTGGAACACACTGAATATT 804
 QY 61 TyrlleuPheAsnleuSerValSerAspLeuAlaPheleuCysThrleuProMetleuIle 80
 |||||
 Db 805 TATCTCTTAACCTCTGCTGTGACTTAACTTTCTGTGGACACCTCCCATGCGATTA 864
 QY 81 ArgSerTyraAlaAsnGlnLysnTrpIleTyGlyAspValleuCysIleSerAsnArgTyra 100
 |||||
 Db 865 AGGAGTTATGCCAATGGAACCTGATATATGAGAGCTGCTCGCTCAAGCAACCATATAT 924
 QY 101 VALLLEHIALAAsnleuTyThrSerileuPheleuThrpheleuSerileaspArg 120
 |||||
 Db 925 GTGCTTCATGCACACCTCATATACGACATTCCTTCTCACTTTATACCATAGATCGA 984
 QY 121 TYRLEUlleileuTyThrProPheArgGluHisleuGlnLysGluPheAlaIle 140
 |||||
 Db 985 TACTGATATTAAGTATACCTTCCGAGAACACCTTCTGCAAAAGAAAGTTGCTATT 1044
 QY 141 LeuileSerleuAlaIleTrpValleuValThrleuGlnleuProilleuProleu 160
 |||||
 Db 1045 TTAATCTCTTGCCCATTTGGGTTTATGAACTGTAGTACTACCATCTTCCCTT 1104
 QY 161 IleasnProvalIleThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyasp 180
 |||||
 Db 1105 ATAAATCCTGTTATACATGACATGACACACCTGTAATGATTTCGCAAGTTCTGAGAC 1164
 QY 181 ProAsnTyraAsnleuIleuTySerMetCysleuThrleuGlnlyPheleuIleProleu 200
 |||||
 Db 1165 CCCAATCAACCTCATTTACAGCATGTGTACACCTGTGGGTTCTTATCTCTT 1224
 QY 201 PheValMetCysPhePheTyThrIleAlaIlePheleuLysGlnIleArgAsnArgGln 220
 |||||
 Db 1225 TTTTGATGTGTTCTTTATTAACAGATGTGCTCTCTCAAAAGCAGAGAAATGAGCAG 1284
 QY 221 ValAlaThrAlaIleuProleuGlnLysProleuAsnleuValIleMetAlaValAlaIle 240
 |||||
 Db 1285 GTTGCTACTGCTGCTGCTTGAAAGCCTCTCAACTGTGTCAATGAGAGTGTGAAATC 1344
 QY 241 PheSerValProPheThrProTyraHisValMetArgAsnValArgIleAlaSerArgleu 260
 |||||
 Db 1345 TTCTCTGTGTTTAAACACCTATCAAGTATGCGGAATGTAGATGCTTACCCCTG 1404
 QY 261 GlySerTrpLysGlnTyraGlnCysThrGlnValIleAlaSerPheTyThrIleValThr 280
 |||||
 Db 1405 GGGAGTGGAAACAGTATAGTCACATGCGTCATCAACCTCTTATTTTCTTTGGAGAT 1464
 QY 281 ArgProleuAlaPheleuAsnSerValIleasnProvalPheTyThrPheleuGlnIleasp 300
 |||||
 Db 1465 CGGCTTTGGCTTCTTCTGAAGTGTATCAACACCTGCTTCTATTTCTTTGGAGAT 1524
 QY 301 HisPheArgAspMetleuMetAsnGlnleuArgHisAsnPhelYserleuThrSerPhe 320
 |||||
 Db 1525 CACTTCAGGACATGCTGTATGATCAACAGACACACACTTCAAAACCTTACATCTTT 1584
 QY 321 SerArgTrpAlaHisGlnleuLeuLeuSerPheArgGlnLys 334
 |||||

Db 1585 AGCAGATGGCGCTCAGTACTCTACTTTCATTCAGAGAAAG 1626

RESULT 6
AC116026

LOCUS

DEFINITION Homo sapiens 3 BAC RP11-3F11 (Roswell Park Cancer Institute Human BAC library) complete sequence.

ACCESSION AC116026 90343 bp DNA linear PRI 09-APR-2002

VERSION AC116026.1 GI:19697319

KEYWORDS HTG.

SOURCE Homo sapiens.

ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 90343)
Mammalia: Eutheria; Primates; Catarrhini; Homnidae; Homo.
Munuy,D.M., Adams,C., Adio-Oduola,B., Ali-oshan,F.R., Allen,C., Alsbrooks,S.L., Amaralunga,H.C., Are,J.R., Ayale,M., Banks,T., Barbara,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D., Buhay,J., Bowie,S., Brieve,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Delaney,K.R., Davis,C., Davy-Carroll,L., Dederich,D.A., Delnaye,K.R., Delgado,O., Denn,A.L., Ding,X., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Kocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlik,P., Hawes,A., He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B., Homs,I.F., Howard,S., Huber,J., Huijck,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtharge,O., Lieu,C., Liu,J., Liu,W., Loulsegad,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,K., Ma,J., Maheshwari,M., Mapa,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhinney,E., McLeod,M.P., Meador,M., Mel,G., Metzker,M., Miner,G., Miner,T., Mitchell,T., Mohabdt,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nickerson,E., Nwokenko,S., Oguh,M., Okunnu,G., Oragunye,N., Oyedero,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojudoan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S., Scott,G., Shen,H., Shooshart,N., Sisson,I., Sodergren,E., Sonalke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Taylor,T., Teitrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalton,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczek,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstein,G. and Gibbs,R.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 90343)
Worley,K.C.

AUTHORS

TITLE Direct Submission

JOURNAL Submitted (23-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 90343)
Worley,K.C.

AUTHORS

TITLE Direct Submission

JOURNAL Submitted (09-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality_info/genbank_annotation.html.

QUALSTAT-REPORT.

FEATURES	QUALSTAT-REPORT.
source	location/Qualifiers
	1. 90343
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/chromosome="3"
	/clone="RP11-3F11"
	991. 1106
repeat_region	/rpt_family="MER45B"
	complement(1314..1627)
repeat_region	/rpt_family="AluSx"
	complement(2137..2430)
repeat_region	/rpt_family="AluY"
	complement(12568..2741)
repeat_region	/rpt_family="L1M4"
	complement(2742..3047)
repeat_region	/rpt_family="AluSx"
	complement(3048..3165)
repeat_region	/rpt_family="L1M4"
	4735..4865
repeat_region	/rpt_family="FLM_C"
	5657..5762
repeat_region	/rpt_family="L1MC/D"
	5906..6237
repeat_region	/rpt_family="LTR21B"
	6289..6773
repeat_region	/rpt_family="HERVFN1"
	complement(8725..9597)
STS	/rpt_family="MER11D"
	12399..12689
repeat_region	/standard_name="136046"
	13774..13816
repeat_region	/rpt_family="Alu"
	13817..13874
repeat_region	/rpt_family="(TA)n"
	complement(15157..15633)
repeat_region	/rpt_family="L2"
	15706..15747
repeat_region	/rpt_family="AT-rich"

repeat_region 16025..16235
/rpl_family="MIR"
repeat_region 16560..16682
/rpl_family="L2"
repeat_region complement(16710..17265)
/rpl_family="LTR49"
repeat_region 18077..18368
/rpl_family="AlusX"
repeat_region complement(18376..18471)
/rpl_family="L2"
repeat_region complement(18486..18659)
/rpl_family="MER57B"
repeat_region complement(20618..20922)
/rpl_family="AlusX"
repeat_region 21337..21363
/rpl_family="AT_rich"
repeat_region 22155..22561
/rpl_family="L1M4"
repeat_region complement(22608..22659)
/rpl_family="L1M4"
repeat_region 22685..23013
/rpl_family="L1M8"
repeat_region 23103..23399
/rpl_family="Alus9"
repeat_region 23500..23973
/rpl_family="L1M3A"
repeat_region complement(24027..24305)
/rpl_family="L1M1"
repeat_region 24304..24655
/rpl_family="L1M3A"
repeat_region 24656..24697
/rpl_family="MADE1"
repeat_region 25203..25518
/rpl_family="AluJo"
repeat_region 25783..25817
/rpl_family="(TAA)n"
repeat_region 26187..26211
/rpl_family="AT_rich"
repeat_region 27014..27030
/rpl_family="AT_rich"
repeat_region complement(27031..27316)
/rpl_family="AlusX"
repeat_region 27317..27328
/rpl_family="AT_rich"
repeat_region 27574..27615
/rpl_family="(TAGA)n"
repeat_region 28062..28166
/standard_name="24707"
STS 28199..28382
/standard_name="13170"
repeat_region complement(29079..29167)
/rpl_family="MT1J"
repeat_region 29168..29532
/rpl_family="THE1B"
repeat_region complement(29533..29552)
/rpl_family="MT1J"
repeat_region 29807..30387
/rpl_family="L1PB2"

Alignment Scores:

Pred. No.: 2.38e-128 Length: 90343
Score: 1713.00 Matches: 328
Percent Similarity: 99.70% Conservative: 0
Best Local Similarity: 99.70% Mismatches: 1
Query Match: 98.05% Indels: 0
DB: 9 Gaps: 0

US-09-765-034-2 (1-334) x AC116026 (1-90343)

Oy 6 AlATpAsnAlAThCysLysAsnTrpLeuAlaIaGlAlaIaLeuGlnLysTyr 25
DB 80665 GCATGGAATGCACACTTGCGCTGGCGACGAGGCTGCCCTGGAATAAGTACTAC 80724

Oy 26 LeuSerIlePheTygIleGluPheValIaGlyValLeuGlyAsnThrIleVal 45
DB 80725 CTTTCATTTTATATGAGATGAGTTCGTGGAGGCTCTTGGAATAACATTTGTT 80784
Oy 46 TyrGlyTyrIlePheSerIleuAsnTrpAsnSerSerAsnIleTyrIleuPheAsnIleu 65
DB 80785 TACGGCTACATCTTCTCTGGAAGAACTGGAACAGCAATATATATCTTTAACTTC 80844
Oy 66 SerValSerAspLeuAlaPheLeuCysThrIleuProMetIleIaGlySerIleAsn 85
DB 80845 TCTGTCTCGACTTACCTTTCTGTGCACCTCCCATCTGATAGAGATTATGCCAT 80904
Oy 86 GlyAsnTrpIleTyrGlyAspValLeuGlyIleSerAsnArgTyrValIleuHisAlaAsn 105
DB 80905 GGAACATGATATATGAGACAGCGCTCGCATATAGCAACCGAATATGCTTCATGCCAAC 80964
Oy 106 LeuTyrThrSerIleleuPheLeuThrPheIleSerIleAspArgTyrIleIleIlys 125
DB 80965 CCTATACACGCAATCTCTCTTCATCTTTATCAGCATATGATATCTGATTAATTAAG 81024
Oy 126 TyrProPheArgGluHisIleuLeuGlnLysGluPheAlaIleleuIleSerLeuAla 145
DB 81025 TATCCTTCGAGAACACCTTCGCAAAAGAAAGATTGCTATATTAATCTCTGGCC 81084
Oy 146 IleTrpValIleuValThrLeuGluLeuLeuProIleLeuProleuIleAsnProValIle 165
DB 81085 ATTTGGGTTTATAGTATACCTTAGAGTTACCATCTTCCCTTATATCTGTTATA 81144
Oy 166 ThrAspAsnGlyThrThrCysAsnAspPheAlaSerSerGlyAspProAsnTyrAsnIleu 185
DB 81145 ACTGACAAATGGACACCCGTAATGATTTTGCAGAGTTGAGAACCCCACTACACATC 81204
Oy 186 IleTyrSerMetCysLeuThrIleuLeuGlyPheIleIleProleuPheValMetCysPhe 205
DB 81205 ATTTACAGCATGTCTTAACACTGTGGGCTCTTATTCCTCTTGTGTGATGTCTTTC 81264
Oy 206 PheTyrTyrIysIleAlaIleuPheLeuLysGlnArgAsnArgGlnValIaThrAlaLeu 225
DB 81265 TTTTATATACAGATGCTCTCTCTCCAAAGCAGAGCAATAGGACAGGTTCTACTGCTGC 81324
Oy 226 ProLeuGluLysProLeuAsnLeuValIleMetAlaValIaIlePheSerValProPhe 245
DB 81325 CCCCTTGAAAGCCTCTCAACTGTGCATCATGAGTGTGATATCTTCTGTGCTTTT 81384
Oy 246 ThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGln 265
DB 81385 ACAACCTATACAGTCACTGCGGAATGTGAGGATGCTTACGCTGCGGAGTTGGAAGCAG 81444
Oy 266 TyrGlnCysThrGlnValValIleAsnSerPheTyrIleValThrArgProleuAlaPhe 285
DB 81445 TATCAGTGACACAGCTGCTCATCAACTCTTTTACATTTGTACACAGGCTTTGGCCTTT 81504
Oy 286 LeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPheArgAspMet 305
DB 81505 CTGAACAGGTGATCAACACCTGCTCTTCTATTTCTTTGGAGATCACTTACGGGACAG 81564
Oy 306 LeuMetAsnGlnLeuArgHisAsnPheLysSerIleuThrSerPheSerArgTrpAlaHis 325
DB 81565 CTGATGAATCAACTGAGACAACTTCAATCCCTTACATCTTTAGCAGATGGGCTCAT 81624
Oy 326 GluLeuLeuLeuSerPheArgLys 334
DB 81625 GAACCTCTACTTTCATTCAGAGAAAAAG 81651
RESULT 7
AC068647
LOCUS: AC068647 132745 bp DNA linear PRI 24-JUL-2002
DEFINITION Homo sapiens 3 BAC RP11-64D22 (Roswell Park Cancer Institute Human
ACCESSION AC068647
VERSION AC068647.10 GI:19774263
KEYWORDS HTG.
SOURCE Homo sapiens.

ORGANISM	Homo sapiens
REFERENCE	1 (bases 1 to 132745)
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayale,M., Banks,T., Barbilora,J., Benton,J., Bimaga,K., Blankenburg,K., Bonini,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M., D., Dathorne,S.R., David,R., Devalla,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwalte,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,T., Foster,P., Frantz,P., Gebisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Correll,J.H.H., Guevara,M., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Haylak,P., Hawes,A., He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hughes,M., Holloway,C., Hollins,B., Homsl,F., Howard,S., Huber,T., Huik,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Ilen,C., Liu,J., Liu,W., Louisege,H., Lozado,R.T., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawlinney,E., McLeod,M.P., Meador,M., Mei,G., Metker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Ogun,M., Okunodu,G., Ogaunye,N., Oviedo,R., Pace,A., Payton,B., Peety,J., Perez,L., Peters,L., Plickens,A., Pridmore,I., Rolfe,M., Ruiz,S., Savory,G., Scherer,S., Rojas,A., Rojoudokan,I., Rolfe,M., Ruiz,S., Savory,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodegren,E., Sonlake,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Syatek,A., Tabot,P., Tameisa,A., Tameisa,K., Tang,H., Tansey,T., Taylor,C., Taylor,T., Tellrod,B., Thomas,N., Thomas,S., Usmani,K., Vazquez,L., Vera,V., Vallalton,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S., Williams,G., Williamson,A., Wleczynk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstein,G. and Gibbs,R.
TITLE	Direct Submission
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 132745)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (06-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	3 (bases 1 to 132745)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (26-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	4 (bases 1 to 132745)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (28-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	5 (bases 1 to 132745)
AUTHORS	Worley,K.C.
TITLE	Direct Submission
JOURNAL	Submitted (29-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE	6 (bases 1 to 132745)
AUTHORS	Worley,K.C.

```

REFERENCE TITLE Direct Submission
AUTHORS Human Genome Sequencing Center, Department
JOURNAL Submitted (25-JUN-2002) of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
7 (bases 1 to 132745)
Morley,K.C.
Direct Submission
Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Mar 20, 2002 this sequence version replaced g1:19718616.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
gc-help@bcm.tmc.edu

COMMENT
CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:
STS are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green
unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

QUALSTAT-REPORT
Location/Qualifiers
1. 132745
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-64D22"
1. 2005
/note="overlaps bases 170209..172213 of clone AC069067"
/function="clone overlap"
30. 130
/standard_name="74493"
complement(522..1015)
/rpt_family="MLT1D"
complement(2452..2697)
/rpt_family="L1MA5A"
complement(3200..3578)
/rpt_family="MLT1B"
3600..3749
/rpt_family="(TA)n"
4391..4411
/rpt_family="AT_rich"
4909..4960
/rpt_family="AT_rich"
complement(5657..6403)

```



```
* 13141 13829: contig of 689 bp in length
* 13830 13929: gap of 100 bp
* 13930 14647: contig of 718 bp in length
* 14648 14747: gap of 100 bp
* 14748 15451: contig of 704 bp in length
* 15452 15551: gap of 100 bp
* 15552 16247: contig of 696 bp in length
* 16248 16347: gap of 100 bp
* 16348 17028: contig of 681 bp in length
* 17029 17128: gap of 100 bp
* 17129 17802: contig of 674 bp in length
* 17803 17902: gap of 100 bp
* 17903 18593: contig of 691 bp in length
* 18594 18693: gap of 100 bp
* 18694 19375: contig of 682 bp in length
* 19376 19475: gap of 100 bp
* 19476 20082: contig of 607 bp in length
* 20083 20182: gap of 100 bp
* 20183 20875: contig of 693 bp in length
* 20876 20975: gap of 100 bp
* 20976 21650: contig of 675 bp in length
* 21651 21750: gap of 100 bp
* 21751 22427: contig of 677 bp in length
* 22428 22527: gap of 100 bp
* 22528 23238: contig of 711 bp in length
* 23239 23338: gap of 100 bp
* 23339 24028: contig of 690 bp in length
* 24029 24128: gap of 100 bp
* 24129 24803: contig of 675 bp in length
* 24804 24903: gap of 100 bp
* 24904 25603: contig of 700 bp in length
* 25604 25703: gap of 100 bp
* 25704 26357: contig of 654 bp in length
* 26358 26457: gap of 100 bp
* 26458 27140: contig of 683 bp in length
* 27141 27240: gap of 100 bp
* 27241 27946: contig of 706 bp in length
* 27947 28046: gap of 100 bp
* 28047 28734: contig of 688 bp in length
* 28735 28834: gap of 100 bp
* 28835 29536: contig of 702 bp in length
* 29537 29636: gap of 100 bp
* 29637 30324: contig of 688 bp in length
* 30325 30424: gap of 100 bp
* 30425 31130: contig of 706 bp in length
* 31131 31230: gap of 100 bp
* 31231 31910: contig of 680 bp in length
* 31911 32010: gap of 100 bp
* 32011 32691: contig of 681 bp in length
* 32692 32791: gap of 100 bp
* 32792 33482: contig of 691 bp in length
* 33483 33582: gap of 100 bp
* 33583 34274: contig of 692 bp in length
* 34275 34374: gap of 100 bp
* 34375 35081: contig of 707 bp in length
* 35082 35181: gap of 100 bp
* 35182 35861: contig of 680 bp in length
* 35862 35961: gap of 100 bp
* 35962 36660: contig of 699 bp in length
* 36661 36760: gap of 100 bp
* 36761 37447: contig of 687 bp in length
* 37448 37547: gap of 100 bp
* 37548 38243: contig of 696 bp in length
* 38244 38343: gap of 100 bp
* 38344 39034: contig of 691 bp in length
* 39035 39134: gap of 100 bp
* 39135 39813: contig of 679 bp in length
* 39814 39913: gap of 100 bp
* 39914 40597: contig of 684 bp in length
* 40598 40697: gap of 100 bp
* 40698 41392: contig of 695 bp in length
* 41393 41492: gap of 100 bp
* 41493 42190: contig of 698 bp in length
```

```
* 42191 42290: gap of 100 bp
* 42291 42967: contig of 677 bp in length
* 42968 43067: gap of 100 bp
* 43068 43736: contig of 669 bp in length
* 43737 43836: gap of 100 bp
* 43837 44525: contig of 689 bp in length
* 44526 44625: gap of 100 bp
* 44626 45306: contig of 681 bp in length
* 45307 45406: gap of 100 bp
* 45407 46111: contig of 705 bp in length
* 46112 46211: gap of 100 bp
* 46212 46848: contig of 637 bp in length
* 46849 46948: gap of 100 bp
* 46949 47639: contig of 691 bp in length
* 47640 47739: gap of 100 bp
* 47740 48431: contig of 692 bp in length
* 48432 48531: gap of 100 bp
* 48532 49221: contig of 690 bp in length
* 49222 49321: gap of 100 bp
* 49322 50017: contig of 696 bp in length
* 50018 50117: gap of 100 bp
* 50118 50799: contig of 682 bp in length
* 50800 50899: gap of 100 bp
* 50900 51583: contig of 684 bp in length
* 51584 51683: gap of 100 bp
* 51684 52384: contig of 701 bp in length
* 52385 52484: gap of 100 bp
* 52485 53167: contig of 683 bp in length
* 53168 53267: gap of 100 bp
* 53268 53966: contig of 699 bp in length
* 53967 54066: gap of 100 bp
```

Alignment Scores:

```
Pred. No.: 2,31e-59 Length: 60298
Score: 861.00 Matches: 157
Percent Similarity: 85.71% Conservative: 29
Best Local Similarity: 72.35% Mismatches: 31
Query Match: 49.28% Gaps: 0
Index: 2
```

US-09-765-034-2 (1-334) x AC116149 (1-60298)

```
QY 14 TTPleuAlaIaGluaIaLeuCluIuSyrIyRleuSerIlePheTyGlyIleGlu 33
Db 3910 TGGGGAATTCAGGCTATCTTGAATAGTACCTCTGATTTATGACATCGAG 3969
QY 34 PheValValGIValIleuGlyAsnThrIleValIyRyGlyIlePheSerIleuS 53
Db 3970 TTCAATTTTGGACACGCTCTGGAATGTCACGTGGCTTGGCTTCTTCATCGAG 4029
QY 54 AsnTrpAsnSerAsnIleTyRleuPheAsnIleuSerValSerAspLeuAlaPhe 73
Db 4030 AACTGGAAACACACCAATGCTATCTTTTAACCTTCCATCTTGACTTGCCTCG 4089
QY 74 CysThrIleuPrometIleuIleArgSerTyRAlaAsnGlyAsnTrpIleTyGly 93
Db 4090 TGCACCCCTCCCATCTGATTAAGAGTATGCCAATGATGAAGGACCACTATGAGAGT 4149
QY 94 LeuGlyIleSerAsnArgTyRValIleuHIsAlaIleuTyRTrpSerIleuPhe 113
Db 4150 CTCGTATTAACCAACCGATATGCTTACACCAACCTTACACACGATCTTCTTC 4209
QY 114 ThrPheIleSerIleAspArgTyRleuIleIleIleTyRTrpPheArgGluHIs 133
Db 4210 ACTTTCATTAACCAACCGATATGCTTACCAAGTATGCCCTTCCGAGACACTTCT 4269
QY 134 GlnIySyrGluPheAlaIleuIleIleSerIleuAlaIleTyRValIleuValTh 153
Db 4270 CAAAGAAGGAATTTGCAATTTATCTCGCTGCTGCTGAGGCTTATGATCAGTGA 4329
QY 154 LeuIleuProIleuProIleuIleAsnProValIleThrAspAsnGlyThThC 173
Db 4330 GTTCTACCACTGCTCATTCTTATCTATCTCTCCCAAGAAGGACGATTAAGTGCAT 4389
```


QY	191	LeuThrLeuLeuGlyPheLeuLeuIleProLeuPheValMet-----CysPhePheTyrTyr	208
Db	1280	ACGACTGGGCCCATGTTGCACTCCCTGGTGTGCATCTGGGCGCTGTATGATTAATT	1339
QY	209	LysIleAlaLeuPheLeuLysGlnIrrAsnArgrGlnValAlaThrAlaLeuProLeu---	227
Db	1340	GTTAGAGCTTTGATCTACAAAGATCTGCACAACCT-----CCTCTCCGG	1384
QY	228	GluLysProLeuAsnLeuValIleMetLeuAlaValIlePheSerValPProPheThrPro	247
Db	1385	AGGAATACCATTTACCTGCTGATTAATTCCTGCAGCGGTTGGCTGTCTTACATCCCT	1444
QY	248	TyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySerTrpLysGlnTyrGln	267
Db	1445	TTCCATGTGATGAATAACATGATTAATTTGAGGCGACGCTG-----GATTTCCAG	1492
QY	268	CysThrGlnValVal-----IleAsnSerPheTyrIleValThrArgPro	282
Db	1493	ACCCAGAAATGTGTGATTTCAACAGCAGCGTTTATGCCACTATACAGTTAAACAAGAGCT	1552
QY	283	LeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeuLeuGlyAspHisPhe	302
Db	1553	CTAGCAATCTCAACACGCTGTGGACCCCATTTCTTATTTCTTGCGCGAGATACATTC	1612
QY	303	ArgAspMetLeuMetAsnGlnLeuArg	311
Db	1613	AGAAAGAGACTGTCTCCGACCAACCAAGG	1639
RESULT 14			
LOCUS	MMU22829	1293 bp	mRNA linear
DEFINITION	Mus musculus P2Y purinoceptor mRNA, complete cds.		
ACCESSION	U22829		
VERSION	U22829.1		
KEYWORDS	GI:767870		
SOURCE	Mus musculus.		
ORGANISM	Mus musculus.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus. 1 (bases 1 to 1293)		
AUTHORS	Tokuyama, Y., Hara, M., Jones, E.M., Fan, Z., and Bell, G.I.		
TITLE	Cloning of rat and mouse P2Y purinoceptors		
JOURNAL	Biochem. Biophys. Res. Commun. 211 (1), 211-218 (1995)		
MEDLINE	95298025		
PUBMED	7779087		
REFERENCE	2 (bases 1 to 1293)		
AUTHORS	Bell, G.I.		
TITLE	Direct Submmission		
JOURNAL	Submitted (14-MAR-1995) Graeme I. Bell, Howard Hughes Medical Institute, University of Chicago, 5641 South Maryland Avenue, Chicago, IL 60637, USA		
FEATURES	location/Qualifiers		
source	1. .1293		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
	/cell_line="M1N6 Insulinoma cells"		
	32. .1153		
	/codon_start=1		
	/product="P2Y purinoceptor"		
	/protein_id="AA91302.1"		
	/db_xref="GI:767871"		
	/translation="MTVEPMSVYPNGIDAAFLAGLGSILKGNSTVASTAAVSSFOCALKTGEFRTYLPAYITLITGLGNSVALIMFVFMKPMWSGISVYENMLADFLVLTLPALFYFNKTDWITIGDAMCKLQRFIFVNTYGSILFLTCIAHRYSGVYPLKSLGRKKNAIYVSIVLWLVIVVAISPLIFSGTGRKKRYTCYDTSNDYLRFTYSMCTVAEFCIPLVILIGCGYILVALIYVALINDVNSLPKRSISYIIVLVEAVSYIPFHVMTNMLRARIDQPEMCDENDRVATVATQVIRGLASINSCVDPIIYFLAGTFFRRLSRTRKASRSRSEANLQSKSEKMTINLSFKONGDSTL"		
CDS			
BASE COUNT	303 a 312 c 311 g 367 t		
ORIGIN			

Pred. No.:	7,78e-32	Length:	1293
Score:	500.00	Matches:	118
Percent Similarity:	54.49%	Conservative:	64
Best Local Similarity:	35.33%	Mismatches:	114
Query Match:	28.62%	Indels:	38
DB:	10	Gaps:	10
US-09-765-034-2 (1-334) x MMU22829 (1-1293)			
Qy	2	LeuGlyIleMetAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaA	17
Db	92	CTGGCTGCGCTTGGGGAACAGATACGTGCTGCACTGACGAGCTTTCCTTCATTC	151
Qy	18	GluaAlaLeuGluys-----TyrTrpLeuSerIlePheTyrGlyLe	32
Db	152	CAATGTGCCCTGACCAACGCGTTTCCAGTTCACCTACCGCGCTGCTACATT	211
Qy	33	GluPheValValGlyValLeuGlyAsnThrIleValValTyrGlyTyrIlePheSer	52
Db	212	GTGTTTCATCATAGGCTTCTTCCGACACGCTGCTATCTGATGTTGTTTCCACATG	271
Qy	53	LysAsnTrpAsnSerSerAsnIleTyrLeuPheAsnLeuSerValSerAspLeuAlaPhe	72
Db	272	AAGCTTGGACGGGATCTCCGTACATGTTCAATTGGCTGCGCTGCTTTTGTAT	331
Qy	73	LeuGlyThrLeuPheMetLeuIleArgSerTyrAlaAsn---GlyAsnTrpIleTyrGly	91
Db	332	GTGCTCACCCCTCACGCGCTCTTCTACATCTTCAACAAGACTGATCTTCGCG	391
Qy	92	AspValLeuGlyIleSerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeu	111
Db	392	GATCTATGTCACAGCGCAGACATCTTCCACGTAATCTCTATGTAAGCATCTTG	451
Qy	112	PheLeuThrPheIleSerIleAspArgTyrLeuIleIleTyrTyrProPheArgGluHis	131
Db	452	TTCCTCACCTGACAGGACAGACAGTGTGCGTGTGTAACCTCCTCAAGTCTCTG	511
Qy	132	LeuLeuGlnLysGluPheAlaIleLeuIleSerLeuAlaIleTyrValLeuValThr	151
Db	512	GCGAGGCTCAAGAAAGAAATGATTTATGTACGCGTGTGCTGCTATGTTGGTG	571
Qy	152	LeuGluLeuLeuProIleLeu-----ProLeuIleAsnProValIle	165
Db	572	GTGGCCATCTCCCTATCTTCTTCTACTCTGCGACCTGGAGCTCGGAAACAAACTGTC	631
Qy	166	ThrAspAsnGlyThrThrCysAsnAspPheAlaSerGlyAspProAsnTyrAsnLeu	185
Db	632	ACCTGATATGACACCGCTCAATGATTAACCTGCGAAGT-----TATTTTC	676
Qy	186	IleTyrSerMetCysLeuThrLeuLeuGlyPheLeuIlePheLeuPheValMet-----	203
Db	677	ATCTACAGATATGTCACAGCTGTGCGCATGTTCTGCACTCCTTGGTCTATCTTGGGC	736
Qy	204	CysPhePheTyrTyrLysIleAlaLeuPheLeuLysGlnArgAsnArgGlnValAlaThr	223
Db	737	TGTTATGATTAATTTAAAGCTTGTGATTACAATGACCTGGACACTCT-----	787
Qy	224	AlaLeuProLeu---GluLysProLeuAsnLeuValIleMetAlaValAlaIlePheSer	242
Db	788	-----CGCGCCGGAGGAATATCATTTACTGGTATTAATTCGTCAGCGTGTTCCT	841
Qy	243	ValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGlySer	262
Db	842	GTGTCTATATCCCTTTCATGATGATAAAGCATGATTTGCGACGCGTTG-----	895
Qy	263	TrpLysGlnTyrGlnCysThrGlnValVal-----IleAsnSerPheTyr	277
Db	896	-----GATTTCCAGACCCCAAGAAATGTCGATTTCAACGACAGGTTTATGCCATTAT	949
Qy	278	IleValThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeu	297
Db	950	CAGTACACAGAGGTCTACGACAGTCTGTGAGCCCATTTCTTATTTCTTG	1009

Qy	298	LeuGlyAspHisPheArgAspMetLeuMetAsnGlnLeuArg	311
Db	1010	GCTGAGATACATTTCGAAGAGACTGTCGCGACGACAGG	1051
RESULT	15		
LOCUS	MMU245636		
DEFINITION	Mus musculus p21 gene for p21 receptor.		
ACCESSION	AJ245636		
VERSION	AJ245636.1 GI:6013074		
KEYWORDS	ADP receptor; P21 gene; P21 receptor.		
SOURCE	Mus musculus.		
ORGANISM	Mus musculus.		
REFERENCE	1 (bases 1 to 12630)		
AUTHORS	Leon, C.		
TITLE	Thromboresistance in p21 receptor knockout mice		
REFERENCE	2 (bases 1 to 12630)		
AUTHORS	Leon, C.		
TITLE	Direct Submission		
JOURNAL	Submitted (04-AUG-1999) LEON C., U311, Inserm, 10 rue Spielmann		
FEATUERS	Submitted (04-AUG-1999) LEON C., U311, Inserm, 10 rue Spielmann		
source	Location/Qualifiers		
	1..12630		
	/organism="Mus musculus"		
	/strain="129/Sv"		
	/sub_species="mus musculus"		
	/db_xref="taxon:10090"		
	/cell_line="ES 129/Sv D3"		
	/dev_stage="embryonic stem cells"		
	3071..11848		
	/gene="p21"		
	3071..4192		
	/gene="p21"		
	/function="ADP receptor"		
	/codon_start=1		
	/product="p21 receptor"		
	/protein_id="CAB57317.1"		
	/db_xref="GI:6013075"		
	/translation="MTEPWSVYVNGDAEFLAGISLMGNSVASTRAVSSFOCAL		
	TKRFOYIYPAVYIITLITIGFLGNSVAIMKVFHMKPWSGISVYHNLADFLYL		
	TLPALIYFNKDWIFGDAMCKLQRIIFHNVLGSLIFLTCISAHRYSGVVPKLK		
	GRUKKNAIVSVLWLVVVAISPIFYSGTGRKKRYCYDTSTNDYLRSEIYS		
	MCTVAFCIPDIVILGCGLYVALIYNDLNSPLRRKSIYIVIVYFAVSYIPF		
	HVKRTNMLRARLDFOPEMCDENDRVATROVTGSLNSCVDPILYFLAGDFRRR		
	LSRATRKASRRSEANLQSKSEMTNLITSEFKONGDRL"		
	4401..4406		
	/gene="p21"		
	4611..4617		
	/gene="p21"		
	9721..9727		
	/gene="p21"		
	10610..10615		
	/gene="p21"		
	10636..10641		
	/gene="p21"		
	11842..11848		
	/gene="p21"		
BASE COUNT	3498 a 2450 c 2763 g 3918 t	1	others
ORIGIN			
Alignment Scores:			
Pred. No.:	8.89e-31	Length:	12630
Score:	500.00	Matches:	118
Percent Similarity:	54.49%	Conservative:	64
Best Local Similarity:	35.33%	Mismatches:	114
Query Match:	28.62%	Indels:	38
DB:	10	Gaps:	10
US-09-765-034-2 (1-334) x MMU245636 (1-12630)			

```
OY      2 LeuGIYIleMeTAlaTrpAsnAlaThrCysLysAsnTrpLeuAlaAla----- 17
      ||||| :|:| :|:|:|:|:|
Db      3131 CTGGGCTGGCTTTGGGGAACAGTACTGCGCTCACTGCACAGCACTTCCCTTCATTC 3190
OY      18 GluAlaAlaLeuGIuLys-----TyrTrpLeuSerIlePheTyrGIlyle 32
      :|:| :|:| :|:| :|:|:|:|
Db      3191 CAATGTGCCCTTACCAAGACGGTTCCAGTCTACTACTACCGGCTGTCTACATTTA 3250
OY      33 GluPheValAlGIyValLeuGIyAsnThrIleValValTyrGIyTrpIlePheSerLeu 52
      |||||:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3251 GTTTCATCATATAGCTTCCCTAGCAACAGCGTGGCTATCTGGATGTTCCGTTTCCACATG 3310
OY      53 LysAsnTrpAsnSerSerSerIleTyrLeuPheAsnLeuSerValSerAspLeuAlaPhe 72
      |||||:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3311 AAGCCTTGGAGCGGCAATCCGTGTACATGTTCAATTGGCTGCTGGCTGCTATTTTATAC 3370
OY      73 LeuCysThrLeuPrometLeuIleArgSerTyrAlaAsn---GlyAsnTrpIleTyrGIy 91
      :|:| :|:|:|:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3371 GTGCTCACCTTACCAAGCCCTCATCTTCTACTACTTCAACAGACTGATCTTGGG 3430
OY      92 AspValLeuCysIleSerAsnArgTyrValLeuHisAlaAsnLeuTyrThrSerIleLeu 111
      ||| :|:|:|:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3431 GATGCTATGTCAGACTGCAGAGATTCACTTCCACGTAAATCTTACGCTAGCATCTTG 3490
OY      112 PheLeuThrPheIleSerIleAspArgTyrLeuIleIleIleTyrTrpPheArgGIuHis 131
      |||||:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3491 TTCCCTACCTGCATCAGCGCACAGAGTACAGTGGCGGTGATCCCTCAAGTCTCTG 3550
OY      132 LeuLeuGIuLysGIuPheAlaIleLeuIleSerLeuAlaIleTyrValLeuValThr 151
      |||||:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3551 GCGAGGCTCAAGAGAAGAAATGCATTATATGACAGCGTGTGCTGCTCATTTGGTGTG 3610
OY      152 LeuGIuLeuLeuProIleLeu-----ProleuIleAsnProValIle 165
      :|:| :|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3611 GTGGCCATCTCCCTATCTCTTCTACTGCGACTGCGAGTGGAAACAAACTGTC 3670
OY      166 ThrAspAsnGIYThrThrCysAsnAspPheAlaSerSerGIYAspProAsnTyrAsnLeu 185
      ||| :|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3671 ACCCTGCTATGACACCACTGCATGATTTACCTGCGAAGT-----TATTTTC 3715
OY      186 IleTyrSerMetCysLeuThrLeuLeuGIYpHeuIleProleuPheValMet----- 203
      |||||:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3716 ATCTACAGATATGTCACGCTGTGGCATGTCTGATCTTGTGCTGATCTTGGGC 3775
OY      204 CysPhePheTyrTyrLysIleAlaLeuPheLeuLysGIuArgAsnArgGIuValAlaThr 223
      |||||:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3776 TGTATGATTAATGTAAAGCTTTGATTTACAATGACCTGGACAACCT----- 3826
OY      224 AlaLeuProLeu---GIuLysProLeuAsnLeuValIleMetAlaValAllePheSer 242
      |||||:|:| :|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3827 -----CCGCTCCGAGGAAATCCATTTACCTGGATGATTAATCTCCTGACGGTGGTTCG 3880
OY      243 ValProPheThrProTyrHisValMetArgAsnValArgIleAlaSerArgLeuGIYSer 262
      ||| :|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3881 GTGTCTTATATCCCTTTCATCTGATGAAACGATGAATTTGGAGACAGGTTG----- 3934
OY      263 TyrLysGIuTyrGIuCysThrGIuValIle-----IleAsnSerPheTyr 277
      :|:|:|:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3935 -----GATTTCCAGACCCCAAGAAATGTGTATTCACAGACAGGTTTATGCCACTTAA 3988
OY      278 IleValThrArgProLeuAlaPheLeuAsnSerValIleAsnProValPheTyrPheLeu 297
      |||||:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3989 CAGGTAACAAAGAGTCTACCAAGTCTCAACAGCTGTGGACCCCATTCCTTATTTCTTG 4048
OY      298 LeuGIYAspHisPheArgAspMetLeuMetAsnGIuLeuArg 311
      |||||:|:| :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      4049 GCTGAGATACATTGAGAAAGAGACTGTCCGAGCCACCAGG 4090
```

THIS PAGE BLANK (USPTO)